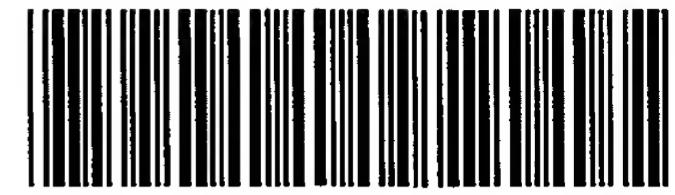# Raw Sequence Listing Error Summary

---

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _10/662,786_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
     Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                       prevent "wrapping."

2 _____ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
     Numbering   use **space characters**, instead.

4 _____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                       ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
                       each n or Xaa can only represent a single residue.** Please present the maximum number of each
                       residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
     "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                       previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                       the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
                       Artificial or Unknown sequences.**

7 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
     (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                       (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                       (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                       This sequence is intentionally skipped

                       Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence.
     (NEW RULES)   <210> sequence id number
                       <400> sequence id number
                       000

9 _____ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
     (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                       In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
     Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
                       is Artificial Sequence

11 _____ Use of <220>   Sequence(s) _1-4_ missing the <220> "Feature" and associated numeric identifiers and responses.
                       Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                       "Unknown." Please explain source of genetic material in <220> to <223> section.
                       (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
     "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                       listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa   "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

OIPE

RAW SEQUENCE LISTING   DATE: 09/25/2003
PATENT APPLICATION: **US/10/662,756**   TIME: 16:04:46

Input Set : **A:\REG660AZ.txt**
Output Set: **N:\CRF4\09252003\J662756.raw**

```
       4 <110> APPLICANT: Economides et al.
       6 <120> TITLE OF INVENTION: DCR-5 BONE AFFECTING LIGAND
       8 <130> FILE REFERENCE: REG 660-A-PCT
C-->  10 <140> CURRENT APPLICATION NUMBER: US/10/662,756
C-->  11 <141> CURRENT FILING DATE: 2003-09-15
      13 <150> PRIOR APPLICATION NUMBER: 60/097,296
      14 <151> PRIOR FILING DATE: 1998-08-20
      16 <160> NUMBER OF SEQ ID NOS: 21
      18 <170> SOFTWARE: FastSEQ for Windows Version 3.0
      20 <210> SEQ ID NO: 1
      21 <211> LENGTH: 27
      22 <212> TYPE: DNA
      23 <213> ORGANISM: Artificial Sequence
      25 <220> FEATURE:
      26 <221> NAME/KEY: misc_feature
      27 <222> LOCATION: 3, 12, 18
      28 <223> OTHER INFORMATION: n = A, T, C or G
      30 <400> SEQUENCE: 1
W-->  31  mgn aar tay ytn aar wsn gay tgg tgy
      33 <210> SEQ ID NO: 2
      34 <211> LENGTH: 24
      35 <212> TYPE: DNA
      36 <213> ORGANISM: Artificial Sequence
      38 <220> FEATURE:
      39 <221> NAME/KEY: misc_feature
      40 <222> LOCATION: 6, 9, 12, 21
      41 <223> OTHER INFORMATION: n = A, T, C or G
      43 <400> SEQUENCE: 2
W-->  44  caracngtnw sngargargg ntgy
      46 <210> SEQ ID NO: 3
      47 <211> LENGTH: 21
      48 <212> TYPE: DNA
      49 <213> ORGANISM: Artificial Sequence
      51 <220> FEATURE:
      52 <221> NAME/KEY: misc_feature
      53 <222> LOCATION: 1, 4, 10, 13, 16
      54 <223> OTHER INFORMATION: n = A, T, C or G
      56 <400> SEQUENCE: 3
W-->  57  nggnggrtcn arnccnggrc a
      59 <210> SEQ ID NO: 4
      60 <211> LENGTH: 24
      61 <212> TYPE: DNA
      62 <213> ORGANISM: Artificial Sequence
```

24

21

Handwritten annotations:
pp 1-3
Does Not Comply
Corrected Diskette Needed
→ needs explanation - see
item 11 on
27 Error
Summary
Sheet

```
 64 <220> FEATURE:
 65 <221> NAME/KEY: misc_feature
 66 <222> LOCATION: 1, 7, 10, (10)  19
 67 <223> OTHER INFORMATION: n = A, T, C or G
 69 <400> SEQUENCE: 4
W--> 70  narrttnacn swcatrcanc krca                              24
 72 <210> SEQ ID NO: 5
 73 <211> LENGTH: 192
 74 <212> TYPE: DNA
 75 <213> ORGANISM: Homo sapiens
 77 <220> FEATURE:
 78 <221> NAME/KEY: CDS
 79 <222> LOCATION: (1)...(192)
 81 <400> SEQUENCE: 5
 82  cag aca gtg acg gag gag ggc tgc cgg agc cgc acc atc ctc aac cgc   48
 83  Gln Thr Val Thr Glu Glu Gly Cys Arg Ser Arg Thr Ile Leu Asn Arg
 84  1               5                  10                  15
 86  ttc tgc tac ggc cag tgc aac tcc ttc tac atc ccg cgg cac gtg aag   96
 87  Phe Cys Tyr Gly Gln Cys Asn Ser Phe Tyr Ile Pro Arg His Val Lys
 88                  20                  25                  30
 90  aag gag gag gag tcc ttc cag tcc tgc gcc ttc tgc aag ccc cag cgc  144
 91  Lys Glu Glu Glu Ser Phe Gln Ser Cys Ala Phe Cys Lys Pro Gln Arg
 92          35                  40                  45
 94  gtc acc tcc gtc ctc gtg gag ctc gag tgc ccg gga cta gac ccc cca  192
 95  Val Thr Ser Val Leu Val Glu Leu Glu Cys Pro Gly Leu Asp Pro Pro
 96      50                  55                  60
 99 <210> SEQ ID NO: 6
100 <211> LENGTH: 64
101 <212> TYPE: PRT
102 <213> ORGANISM: Homo sapiens
104 <400> SEQUENCE: 6
105  Gln Thr Val Thr Glu Glu Gly Cys Arg Ser Arg Thr Ile Leu Asn Arg
106  1               5                  10                  15
107  Phe Cys Tyr Gly Gln Cys Asn Ser Phe Tyr Ile Pro Arg His Val Lys
108                  20                  25                  30
109  Lys Glu Glu Glu Ser Phe Gln Ser Cys Ala Phe Cys Lys Pro Gln Arg
110          35                  40                  45
111  Val Thr Ser Val Leu Val Glu Leu Glu Cys Pro Gly Leu Asp Pro Pro
112      50                  55                  60
116 <210> SEQ ID NO: 7
117 <211> LENGTH: 30
118 <212> TYPE: DNA
119 <213> ORGANISM: Artificial Sequence
121 <220> FEATURE:
122 <223> OTHER INFORMATION: Primer
124 <400> SEQUENCE: 7
125· agc cgc acc atc ctc aac cgc ttc tgc tac                           30
127 <210> SEQ ID NO: 8
128 <211> LENGTH: 10
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/662,756

DATE: 09/25/2003
TIME: 16:04:46

Input Set : **A:\REG660AZ.txt**
Output Set: **N:\CRF4\09252003\J662756.raw**

```
129 <212> TYPE: PRT
130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: Primer
135 <400> SEQUENCE: 8
136  Ser Arg Thr Ile Leu Asn Arg Phe Cys Tyr
137  1               5                   10
139 <210> SEQ ID NO: 9
140 <211> LENGTH: 27
141 <212> TYPE: DNA
142 <213> ORGANISM: Artificial Sequence
144 <220> FEATURE:
145 <223> OTHER INFORMATION: Primer
147 <400> SEQUENCE: 9
148  ctcgagctcc acgaggacgg aggtgac                                    27
150 <210> SEQ ID NO: 10
151 <211> LENGTH: 9
152 <212> TYPE: PRT
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Primer
158 <400> SEQUENCE: 10
159  Glu Leu Glu Val Leu Val Ser Thr Val
160  1               5
162 <210> SEQ ID NO: 11
163 <211> LENGTH: 507
164 <212> TYPE: DNA
165 <213> ORGANISM: Homo sapiens
167 <220> FEATURE:
168 <221> NAME/KEY: CDS
169 <222> LOCATION: (1)...(504)
170 <223> OTHER INFORMATION: 4
173 <400> SEQUENCE: 11
174  atg ttc tgg aag ctt tcc ctg tcc ttg ttc ctg gtg gcg gtg ctg gtg    48
175  Met Phe Trp Lys Leu Ser Leu Ser Leu Phe Leu Val Ala Val Leu Val
176  1               5                   10                  15
178  aag gtg gcg gaa gcc cgg aag aac cgg ccg gcg ggc gcc atc ccc tcg    96
179  Lys Val Ala Glu Ala Arg Lys Asn Arg Pro Ala Gly Ala Ile Pro Ser
180              20                  25                  30
182  cct tac aag gac ggc agc agc aac aac tcg gag aga tgg cag cac cag   144
183  Pro Tyr Lys Asp Gly Ser Ser Asn Asn Ser Glu Arg Trp Gln His Gln
184              35                  40                  45
186  atc aag gag gtg ctg gcc tcc agc cag gag gcc ctg gtg gtc acc gag   192
187  Ile Lys Glu Val Leu Ala Ser Ser Gln Glu Ala Leu Val Val Thr Glu
188          50                  55                  60
190  cgc aag tac ctc aag agt gac tgg tgc aag acg cag ccg ctg cgg cag   240
191  Arg Lys Tyr Leu Lys Ser Asp Trp Cys Lys Thr Gln Pro Leu Arg Gln
192          65                  70                  75                  80
194  acg gtg agc gag gag ggc tgc cgg agc cgc acc atc ctc aac cgc ttc   288
```

FYI: A primer is usually a nucleotide sequence. (handwritten note, with "Primer" on line 133 circled)

see above (handwritten note, with "Primer" on line 156 circled)

RAW SEQUENCE LISTING   DATE: 09/25/2003
PATENT APPLICATION: **US/10/662,756**   TIME: 16:04:46

Input Set : **A:\REG660AZ.txt**
Output Set: **N:\CRF4\09252003\J662756.raw**

```
195    Thr Val Ser Glu Glu Gly Cys Arg Ser Arg Thr Ile Leu Asn Arg Phe
196                    85              90              95
198    tgc tac ggc cag tgc aac tcc ttc tac atc ccg cgg cac gtg aag aag     336
199    Cys Tyr Gly Gln Cys Asn Ser Phe Tyr Ile Pro Arg His Val Lys Lys
200                    100             105             110
202    gag gag gag tcc ttc cag tcc tgc gcc ttc tgc aag ccc cag cgc gtc     384
203    Glu Glu Glu Ser Phe Gln Ser Cys Ala Phe Cys Lys Pro Gln Arg Val
204                    115             120             125
206    acc tcc gtc ctc gtg gag ctc gag tgc ccc ggc ctg gac cca ccc ttc     432
207    Thr Ser Val Leu Val Glu Leu Glu Cys Pro Gly Leu Asp Pro Pro Phe
208            130             135             140
210    cga ctc aag aaa atc cag aag gtg aag cag tgc cgg tgc atg tcc gtg     480
211    Arg Leu Lys Lys Ile Gln Lys Val Lys Gln Cys Arg Cys Met Ser Val
212    145             150             155             160
214    aac ctg agc gac tcg gac aag cag tga                                 507
215    Asn Leu Ser Asp Ser Asp Lys Gln
216                    165
218 <210> SEQ ID NO: 12
219 <211> LENGTH: 168
220 <212> TYPE: PRT
221 <213> ORGANISM: Homo sapiens
223 <400> SEQUENCE: 12
224    Met Phe Trp Lys Leu Ser Leu Ser Leu Phe Leu Val Ala Val Leu Val
225     1           5               10              15
226    Lys Val Ala Glu Ala Arg Lys Asn Arg Pro Ala Gly Ala Ile Pro Ser
227                    20              25              30
228    Pro Tyr Lys Asp Gly Ser Ser Asn Asn Ser Glu Arg Trp Gln His Gln
229            35              40              45
230    Ile Lys Glu Val Leu Ala Ser Ser Gln Glu Ala Leu Val Val Thr Glu
231    50              55              60
232    Arg Lys Tyr Leu Lys Ser Asp Trp Cys Lys Thr Gln Pro Leu Arg Gln
233    65              70              75              80
234    Thr Val Ser Glu Glu Gly Cys Arg Ser Arg Thr Ile Leu Asn Arg Phe
235                    85              90              95
236    Cys Tyr Gly Gln Cys Asn Ser Phe Tyr Ile Pro Arg His Val Lys Lys
237                    100             105             110
238    Glu Glu Glu Ser Phe Gln Ser Cys Ala Phe Cys Lys Pro Gln Arg Val
239                    115             120             125
240    Thr Ser Val Leu Val Glu Leu Glu Cys Pro Gly Leu Asp Pro Pro Phe
241            130             135             140
242    Arg Leu Lys Lys Ile Gln Lys Val Lys Gln Cys Arg Cys Met Ser Val
243    145             150             155             160
244    Asn Leu Ser Asp Ser Asp Lys Gln
245                    165
247 <210> SEQ ID NO: 13
248 <211> LENGTH: 48
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
```

253 <223> OTHER INFORMATION: Primer
255 <400> SEQUENCE: 13
256 cagatagaat tcgccgccac catggtgtgg aagctttccc tgtccttg   48
258 <210> SEQ ID NO: 14
259 <211> LENGTH: 30
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Primer
266 <400> SEQUENCE: 14
267 cacgagaccg gtctgcttgt ccgagtcgct   30
269 <210> SEQ ID NO: 15
270 <211> LENGTH: 114
271 <212> TYPE: DNA
272 <213> ORGANISM: Artificial Sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: Triple myc tag
277 <400> SEQUENCE: 15
278 gagcagaagc tgatatccga agaagacctc ggcggagagc agaagctcat aagtgaggaa   60
279 gacttgggcg gagagcagaa gcttatatcc gaagaagatc tcggaccgtg ataa   114
281 <210> SEQ ID NO: 16
282 <211> LENGTH: 52
283 <212> TYPE: DNA
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: Primer
289 <400> SEQUENCE: 16
290 gagagacatg tctcggaaga accgtccggc tggcgccatc ccctcgcctt ac   52
292 <210> SEQ ID NO: 17
293 <211> LENGTH: 39
294 <212> TYPE: DNA
295 <213> ORGANISM: Artificial Sequence
297 <220> FEATURE:
298 <223> OTHER INFORMATION: Primer
300 <400> SEQUENCE: 17
301 gagagcggcc gctcattact gcttgtccga gtcgctcag   39
303 <210> SEQ ID NO: 18
304 <211> LENGTH: 9
305 <212> TYPE: PRT
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Mammalian
311 <400> SEQUENCE: 18
312 Arg Lys Tyr Leu Lys Ser Asp Trp Cys
313   1   5
315 <210> SEQ ID NO: 19
316 <211> LENGTH: 8
317 <212> TYPE: PRT
318 <213> ORGANISM: Artificial Sequence

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/25/2003
PATENT APPLICATION: **US/10/662,756**   TIME: 16:04:47

Input Set : **A:\REG660AZ.txt**
Output Set: **N:\CRF4\09252003\J662756.raw**

<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 3,12,18
Seq#:2; N Pos. 6,9,12,21
Seq#:3; N Pos. 1,4,10,13,16
Seq#:4; N Pos. 1,7,10,19